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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Jun 08 19:36:04 EDT 2007

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Output Set:

Actual SeqID Count: 19

[illegible]

Input Set:

Output Set:

Started: 2007-06-08 19:35:50.118
Finished: 2007-06-08 19:35:56.264
Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 146 ms
Total Warnings: 15
Total Errors: 26
No. of SeqIDs Defined: 19
Actual SeqID Count: 19

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
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E 257	Invalid sequence data feature in <221> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
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E 257	Invalid sequence data feature in <221> in SEQ ID (19) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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<120> REARRANGED SQUAMOUS CELL CARCINOMA ANTIGEN GENES II

<130> 7274

<140> 10/661,742

<141> 2003-09-12

<150> PCT/SE02/00512

<151> 2002-03-15

<150> SE 0100938

<151> 2001-03-15

<160> 19

<170> PatentIn Ver. 3.3

<210> 1

<211> 390

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
construct

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			20					25					30		

Ser	Ile	Thr	Ser	Ala	Leu	Gly	Met	Val	Leu	Leu	Gly	Ala	Lys	Asp	Asn
		35					40					45			

Thr	Ala	Gln	Gln	Ile	Lys	Lys	Val	Leu	His	Phe	Asp	Gln	Val	Thr	Glu
	50					55					60				

Asn	Thr	Thr	Gly	Lys	Ala	Ala	Thr	Tyr	His	Val	Asp	Arg	Ser	Gly	Asn
65				70					75					80	

Val	His	His	Gln	Phe	Gln	Lys	Leu	Leu	Thr	Glu	Phe	Asn	Lys	Ser	Thr
			85						90					95	

Asp	Ala	Tyr	Glu	Leu	Lys	Ile	Ala	Asn	Lys	Leu	Phe	Gly	Glu	Lys	Thr
		100						105					110		

Tyr	Leu	Phe	Leu	Gln	Glu	Tyr	Leu	Asp	Ala	Ile	Lys	Lys	Phe	Tyr	Gln
		115					120					125			

Thr	Ser	Val	Glu	Ser	Val	Asp	Phe	Ala	Asn	Ala	Pro	Glu	Glu	Ser	Arg
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Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160
 Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
 165 170 175
 Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
 180 185 190
 Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205
 Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
 210 215 220
 Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240
 Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255
 Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270
 Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285
 Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300
 Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
 305 310 315 320
 His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
 325 330 335
 Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
 340 345 350
 Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
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<211> 1193

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

construct

<400> 2

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gctgaagatc gccacaagc tcttcggaga aaaaacgtat ctatttttac aggaatattt 360
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<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 3

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<210> 4

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
primer

<400> 4

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<210> 5

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<210> 7 <211> 19 <212> DNA <213> Artificial Sequence	
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<400> 7 tggagccacg gtctctcag	19
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<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 10
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<210> 11
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
construct

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caagtcacag agaacaccac aggaaaagct gcaacatata atgttgatag gtcaggaaat 240
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ctgaagatcg ccaacaagct cttcggagaa aaaacgtatc tatttttaca ggaatattta 360
gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
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<211> 1173
<212> DNA
<213> Homo sapiens

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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
caagtcacag agaacaccac aggaaaagct gcaacatata atgttgatag gtcaggaaat 240


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gttcatcacc agtttcaaaa gtttctgact gaattcaaca aatccactga tgcataatgag 300
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gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
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<210> 13

<211> 1173

<212> DNA

<213> Homo sapiens

<400> 13

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caagtcacag agaacaccac agaaaaagct gcaacatata atgttgatag gtcaggaaat 240
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gatgccatca agaaatttta ccagaccagt gtggaatcta ctgattttgc aaatgctcca 420
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<210> 14

<211> 390

<212> PRT

<213> Homo sapiens

<400> 14

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Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
 35 40 45

Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
 50 55 60

Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
 65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
 85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
 100 105 110

Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
 115 120 125

Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
 130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
 145 150 155 160

Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
 165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
 180 185 190

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
 195 200 205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
 210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
 225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
 245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
 260 265 270

Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
 275 280 285

Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
 290 295 300

Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
 305 310 315 320

Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
 325 330 335

Thr Glu Glu Gly Ala Glu Ala Ala Ala Thr Ala Val Val Gly Phe
340 345 350

Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
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Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
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Gly Arg Phe Ser Ser Pro
385 390

<210> 15

<211> 390

<212> PRT

<213> Homo sapiens

<400> 15

Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
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Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
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Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
35 40 45

Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
50 55 60

Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65 70 75 80

Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
85 90 95

Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
100 105 110

Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
115 120 125

Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
130 135 140

Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145 150 155 160

Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
165 170 175

Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
180 185 190

Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys

195

200

205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys